47. (New) The method of claim 6, wherein the untranslatable plus-sense RNA molecule, double-stranded RNA molecule, or untranslatable double-stranded RNA molecule is at least 700 base pairs in length and comprises nucleotide residues between positions 1 through 1802 of the nucleic acid sequence as set forth as SEQ ID NO: 10.

C7. cont'd

48. (New) The method of claim 6, wherein the untranslatable plus-sense RNA molecule, double-stranded RNA molecule, or untranslatable double-stranded RNA molecule is at least 700 base pairs in length and comprises a nucleic acid sequence as set forth as SEQ ID NO: 7.

REMARKS

By this amendment, claims 2, 17-24, and 29-40 have been cancelled, with all rights to the encompassed subject matter reserved. New claims 41-48 are added. Claims 1, 3, 6, 7, and 9-11 are amended. Claim 3 is amended to correct its dependency. Claims 1, 6, and 11 are amended to correct form. Support for the amended and new claims can be found in the specification as it was originally filed at least as follows:

Claim	*Support in Specification*
1	Page 4, lines 26-30; page 19, lines 24-26; page 25, lines 17-19; original claim 2.
6	Page 4, lines 26-30; page 19, lines 24-26; page 21, lines 2-3; page 25, lines 17-19; original claims 1 and 2.
7	Page 21, lines 2-3; original claim 1.
9	Page 21, lines 2-3; original claim 1.
10	Page 23, lines 21-25.
11	Page 4, lines 26-30; page 19, lines 24-26; page 21, lines 2-3; page 25, lines 17-19; page 26, lines 26-29; original claims 1 and 2.
41	Page 6, line 1; page 25, lines 9-12; original claim 1.
42	Page 6, line 1; page 25, lines 17-19; original claim 1.
43	Page 6, line 1; page 19, lines 24-26; SEQ ID NO: 10; original claim 1.
44	Page 5, lines 25-26; page 19, lines 24-26; page 27, lines 9-12; original claim 1.
45	Page 6, line 1; page 25, lines 9-12; original claim 1.
46	Page 6, line 1; page 25, lines 17-19; original claim 1.
47	Page 6, line 1; page 19, lines 24-26; SEQ ID NO: 10; original claim 1.
48	Page 5, lines 25-26; page 19, lines 24-26; page 27, lines 9-12; original claim 1.

In addition, subject matter related to a non-elected invention (SEQ ID NO: 11, SEQ ID NO: 12) has been removed from claim 11.

No new matter has been added by any of these amendments. Unless specifically stated otherwise, these amendments are not intended to limit the scope of any claim. Reconsideration of the application in light of the amendments and the following discussion is respectfully requested.

Telephone interview

Applicants thank Examiner Baum and Examiner McElwain for granting their undersigned representative a telephone interview regarding this application on October 8, 2002. Also present at that interview was Anne Carlson, Ph.D. for Applicants.

During that conversation, the rejections of the claims under 35 U.S.C. §102 were discussed extensively, and the rejections under 35 U.S.C. §101, §103 and §112 were discussed briefly. Specific language that might resolve these rejections was discussed, and though final resolution was not reached on all issues during the interview, Applicants believe that the amendments submitted herewith reflect issues discussed in the telephone interview.

In addition, Examiners Baum and McElwain agreed to consider a Declaration describing the superior effect of Applicants' invention, as compared to the system described in Hiroyasu *et al.* (Kokai Number (1993) 68574). Applicants will submit, in a separate communication, a Declaration under 37 C.F.R. 1.132 from Inventor L. Walter Ream, Jr., Ph.D.

Response to Restriction Requirement

Applicants acknowledge that their election of Group I and SEQ ID NO: 10 has been made final by the Examiner. Claim 2 has been cancelled, thus rendering the objection to this claim moot. Claim 11 has been amended to remove the reference to SEQ ID NOs: 11 and 12, which recite the nucleic acid sequences of the *iaaH* and *ipt* genes, respectively. This subject

matter is directed to a non-elected invention. Applicants reserve the right to pursue non-elected Group II (cancelled claims 17-24) during future prosecution.

Applicants acknowledge that the Examiner considers claims 29-40 to be directed to a non-elected invention. Applicants traverse the withdrawal of claims 29-40 from consideration and reserve the right to petition for their consideration during future prosecution, but for the sake of expediting prosecution in the current case have cancelled these claims.

Claim Rejections under 35 U.S.C. §112, First Paragraph

Written Description Requirement

Claims 1-16, and 25-28 stand rejected under 35 U.S.C. §112, first paragraph for allegedly containing subject matter that was not adequately described in the specification. Applicants traverse this rejection.

The Examiner alleges that the claims do not identify structural features unique to genes responsible for causing gall disease and that the claims do not identify structural features unique to the protein encoded by SEQ ID NO: 10, the functional domains of either protein nor the overall function of the proteins. Applicants have amended claims 1, 6, and 11 to more clearly define their invention and include structural features that are unique to the gene responsible for causing gall disease. In particular, claims 1 and 6 are now directed to methods of producing a plant cell or a plant, respectively, that are resistant to gall disease wherein the nucleic acid molecule *encodes an untranslatable plus-sense RNA molecule, a double-stranded RNA molecule, or an untranslatable double-stranded RNA molecule, wherein the RNA molecule is at least 700 base pairs in length and comprises at least one stop sequence, and wherein the gene comprises a nucleic acid sequence as set forth as SEQ ID NO: 10.* Claim 11 is now directed to a recombinant nucleic acid molecule having *at least 90% sequence identity with a gene responsible for causing gall disease, wherein the gene comprises a nucleic acid sequence as set forth as SEQ ID NO: 10, wherein the nucleic acid sequence encodes an untranslatable plus-sense RNA molecule, a*

double-stranded RNA molecule, or an untranslatable double-stranded RNA molecule of at least 700 base pairs in length and comprises at least one stop sequence.

The Examiner also alleges that the claims do not specify the genotype or phenotype of plants transformed with a gene responsible for causing gall disease. As described above, the claims have been amended to specify the genotype of the transformed plant or plant cell. Applicants have amended claims 1, 6, and 11 to more clearly define their invention and include a description of the phenotype of the plant or plant cell transformed with a gene responsible for causing gall disease. In particular, claims 1 and 6 now recite the production of a plant cell or plant, respectively, that is *resistant to gall disease*. Claim 11 now recites a recombinant nucleic acid molecule that *when introduced into and expressed in a plant, makes the plant resistant to gall disease*.

In light of the above amendments, one of skill in the art can readily identify the structural feature of the nucleic acid molecule that is transformed into a plant in order to produce the phenotype of resistance to gall disease. Applicants therefore request that the rejection of claims 1, 6, and 11, and all claims depending from them, be withdrawn.

Enablement Requirement

Claims 1-16 and 25-28 stand rejected under 35 U.S.C. §112, first paragraph for allegedly being enabled for any nucleic acid sequence or fragment thereof responsible for causing gall disease, any polynucleotide that is 60% identical to SEQ ID NO: 10, any number of stop codons in any location of a nucleic acid sequence, or a protein having any level of homology to SEQ ID NO: 10 that is associated with double-stranded RNA degradation. Applicants traverse this rejection. In addition, claims 1, 6, and 11 have been amended to more clearly define Applicants' invention.

Claims broadly drawn to any polynucleotide

As described above, Applicants have amended claims 1, 6, and 11 to more clearly define their invention, thereby rendering moot the rejection of claims broadly drawn to **any** polynucleotide. Applicants respectfully request that the rejection be withdrawn.

Claims drawn to any number of stop codons in any location

Applicants clearly describe in the specification that there exist many methods of rendering an RNA molecule untranslatable (page 14, line 10 – page 17, line 32). Rendering an RNA molecule untranslatable includes the introduction of any of various stop signals into the open-reading frame of the DNA molecule (page 14, lines 13-14) and the DNA molecule can contain one or more premature stop codons (page 14, lines 14-15). Applicants have demonstrated that as few as one stop codon is enough to render the RNA untranslatable. Any additional stop codons generated by a frame-shift introduced into a nucleic acid sequence is considered solely to be a precautionary measure when introducing transgenes into crops and is a technique that is well known to those of ordinary skill in the art. Thus, claims 1, 6, and 11 have been amended to more clearly define their inventions. In particular, claims 1, 6, and 11 recite that the nucleic acid molecule comprises *at least one stop sequence*. Applicants respectfully request that the rejection be withdrawn.

Claims drawn to a mechanism associated with double-stranded RNA degradation that is active at any level of homology

Applicants have demonstrated that the *iaaM* transgene, which is derived from an octopine-type Ti plasmid, is capable of silencing the *iaaM* gene from a nopaline-type Ti plasmid. The octopine- and nopaline-derived iaaM genes have nucleic acid sequences that are 94% identical (**Exhibit A**). Thus, it is clear from Applicants' data that a nucleic acid sequence that is homologous (*i.e.* similar, **but not identical)** to the *iaaM* transgene can be silenced by the transgene. In light of the above, Applicants have amended claims 1, 6, and 11 to more clearly define their invention and include a description of the level of homology of the nucleic acid molecule associated with RNA degradation. In particular, claims 1 and 6 now recite a nucleic

acid molecule that is *at least 90%* homologous to a gene responsible for causing gall disease. In addition, claim 11 now recites a recombinant nucleic acid molecule having *at least 90% sequence identity with a gene responsible for causing gall disease*. In light of these arguments and amendments, the rejection that claims do not specify at what level of homology the mechanism associated with double-stranded RNA degradation is no longer active is moot. Applicants respectfully request that the rejection be withdrawn.

Claim Rejections under 35 U.S.C. §102

102(a)

Claims 11-14 are rejected under 35 U.S.C. §102(a) for allegedly being anticipated by Li *et al.* (12 November, 1998, WO 98/49888, hereinafter the '888 publication). Applicants traverse this rejection.

> 35 U.S.C. §102(a) states that "[a] person shall be entitled to a patent unless-
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for patent..."

Applicants' patent application was filed on November 4, 1999 and, as is stated on lines 5-7 of the specification, claims the benefit of U.S. Provisional Application No. 60/107,185 filed on November 5, 1998. Since Applicants' application has an effective priority date, and therefore a constructive date of invention, that pre-dates the publication date of the '888 publication, the '888 publication is not prior art under §102(a). It is respectfully requested that the Examiner withdraw the §102(a) rejection regarding the '888 publication.

Applicants note, that the '888 publication relates to U.S. Patent No. 6,268,552 (hereinafter the '552 patent), which was filed on May 6, 1998 and therefore has an earlier effective filing date than the Applicants' patent application. A copy of the '552 patent is submitted herewith, in a Supplemental Information Disclosure Statement.

Li *et al.*, in the '552 patent, describes the production of "...transgenic tomato plants which produce elevated levels of plant hormones such as auxin (*e.g.*, via a GH3 promoter driving expression of an (sic) tryptophan oxygenase coding sequence, GH3-iaaM)..." (column 6, lines 49-52). Thus, Li *et al.* teaches that the **expression**, in plant cells, plant tissues, and plants, of the **enzyme** encoded by the *iaaM* gene yields an over-production of auxin. This is in direct contrast to, and in fact teaches away from, Applicants' invention, which is to **inhibit** the expression of the enzyme encoded by the *iaaM* gene thereby reducing the production of auxin (specification, page 3, lines 23 through page 5, line 9).

In light of this obvious distinction, Applicants believe that claims 1-16 and 25-28 are not anticipated by either the '888 publication or the '552 patent, and request that the rejection be withdrawn.

§102(b)

Claims 1-16 and 25-28 stand rejected for allegedly being anticipated by Hiroyasu *et al.* (Kokai Number (1993) 68574). In particular, it is alleged that the Hiroyasu *et al.* reference teaches a method of inhibiting the transformation of tobacco plants by *Agrobacterium* when tobacco leaf disks are transformed with the *iaaM* gene in either the sense or antisense orientation and that this anticipates Applicants' claims. Applicants traverse this rejection.

Applicants have amended claims 1, 6, and 11 to more clearly define their invention. In particular, amended claims 1 and 6 recite a method that includes transforming a plant cell with a nucleic acid molecule that is *at least 90% homologous* to a gene responsible for causing gall disease, wherein the nucleic acid molecule encodes an untranslatable plus-sense RNA molecule, a double-stranded RNA molecule, or an untranslatable double-stranded RNA molecule, wherein the RNA molecule is *at least 700 base pairs in length and comprises at least one stop sequence, and wherein the gene comprises a nucleic acid sequence as set forth as SEQ ID NO: 10.* Amended claim 11 recites a recombinant nucleic acid molecule comprising a nucleic acid sequence having *at least 90% sequence identity with a gene responsible for causing gall disease,*

wherein the nucleic acid sequence encodes an untranslatable plus-sense RNA molecule, a double-stranded RNA molecule, or an untranslatable double-stranded RNA molecule, wherein the RNA molecule is *at least 700 base pairs in length and comprises at least one stop sequence.*

Hiroyasu *et al.* describes a 697 base pair *iaaM* fragment that prevents crown gall disease in tobacco leaf disks. The claims, as amended, recite a method of preventing crown gall disease by transforming plant cells with an *iaaM* fragment that is **larger** than the 697 base pair Hiroyasu *et al.* fragment. Thus, Hiroyasu *et al.* does not describe all of the limitations of the amended claims and the amended claims are not anticipated by Hiroyasu *et al.*

Claims 2-5 depend directly or indirectly from claim 1, and claims 7-10 depend directly or indirectly from claim 6. Claims 12-16 and 25-28 depend directly or indirectly from claim 11. These dependent claims thereby incorporate the amended limitations of claims 1, 6, and 11. In light of these arguments, and the amendments to claims 1, 6, and 11, Applicants request that the rejection of claims 1-16 and 25-28 under §102(b) be withdrawn.

Claim Rejections under 35 U.S.C. §103

Claims 1-14 and 16

Claims 1-14 and 16 stand rejected as allegedly rendered obvious by Hiroyasu *et al.* in light of Hartmann *et al.* (1983, Plant Propagation, 4th edition, Prentice Hall, Inc., Englewood Cliffs, pages 345-349, and 351-358). Applicants traverse this rejection.

As described above, Applicants have amended claims 1, 6, and 11 to more clearly define the claimed invention. In addition, arguments are presented below which clearly illustrate ways in which the claimed invention is distinguishable from the cited publication.

Hiroyasu *et al.* teaches that a specific *iaaM* nucleic acid sequence containing residues between positions 143-840 of the nucleic acid sequence (697 base pair fragment) inhibits tumor growth in a plant when the plant is transformed with the *iaaM* fragment in the sense direction.

Hiroyasu *et al.* only teaches the 697 base pair fragment and does not indicate that plants were transformed with other fragments. Thus, Hiroyasu *et al.* does not teach that **any** *iaaM* fragment, except the 697 base pair fragment, is required to silence *iaaM*. Moreover, since the effect of other *iaaM* fragments was not compared to the effect of the 697 base pair fragment, Hiroyasu *et al.* does not teach that the 697 base pair fragment is the superior fragment in *iaaM* silencing and it provides no teaching or expectation that other fragments would be effective.

Applicants have demonstrated, however, that merely introducing any fragment of an *iaaM* nucleic acid sequence, even one that either contains all or part of the 697 base pair Hiroyasu *et al.* sequence, is not sufficient to *consistently* silence the *iaaM* gene in plants transformed with the fragments. Furthermore, Applicants have demonstrated that the size of the Hiroyasu *et al.* fragment (697 base pairs) does not determine the ability of the fragment to silence *iaaM*, since three different 600 base pair fragments had no silencing effect on *iaaM*.

Applicants have also demonstrated that the 1800 base pair *iaaM* fragment (positions 9-1807 of SEQ ID NO: 7) is highly effective at preventing crown gall tumor growth in tobacco plants (specification at page 27, lines 18-22). When Applicants compared the 1800 base pair fragment to other *iaaM* fragments, only one of the fragments had an effect on *iaaM* silencing, and it's effect was significantly less potent than that of the 1800 base pair fragment. Thus, as a result of the lack of teaching in Hiroyasu *et al.* regarding effective fragments other than the specifically described 697 base pair fragment, combined with the variability in the ability of *iaaM* fragments to silence *iaaM*, one of ordinary skill in the art would not have been able to predict which *iaaM* fragments would be capable of effectively silencing *iaaM* expression. Thus, Hiroyasu *et al.* does not render the currently claimed invention obvious.

Hartmann *et al.* teaches the theory, method and value of grafting plants, however Hartmann *et al.* does not provide explicit or implicit teachings that overcome the shortcomings of the Hiroyasu *et al.* reference. Since all of the limitations of Applicants' invention are not taught by the combination of Hiroyasu *et al.* and Hartmann *et al.*, this combination of references

does not and cannot render the subject matter of claims 1-14 and 16 obvious. Applicants request that the rejection of these claims under §103(a) be withdrawn.

Claims 11-15 and 27

Claims 11-15 and 27 stand rejected as allegedly rendered obvious by Li *et al.* in light of Firoozabady *et al.* (USPN 5,792,927). Applicants traverse this rejection.

As described above, Li *et al.* (either the '888 publication or the '552 patent) teaches that the expression, in plant cells, plant tissues, and plants, of the enzyme encoded by the *iaaM* gene yields an over-production of auxin, and thus Li *et al.* teaches away from Applicants' invention. Li *et al.* therefore does not teach the suppression of *iaaM* in order to prevent a disease caused by *Agrobacterium.*

Firoozabady *et al.* teaches a method of rose transformation, however Firoozabady *et al.* does not provide explicit or implicit teachings that overcome the shortcomings of the Li *et al.* reference. Since all of the limitations of Applicants' invention are not taught by the combination of Li *et al.* and Firoozabady *et al.*, this combination of references does not and cannot render the subject matter of claims 11-15 and 27 obvious. Applicants request that the rejection of these claims under §103(a) be withdrawn.

Claims 11-14 and 25

Claims 11-14 and 25 stand rejected as allegedly rendered obvious by Li *et al.* in light of Lemieux (USPN 5,567,599). Applicants traverse this rejection.

As described above, Li *et al.* does not teach the suppression of *iaaM* in order to prevent a disease caused by *Agrobacterium.* Lemieux teaches a method of chrysanthemum transformation but does not provide explicit or implicit teachings that overcome the shortcomings of the Li *et al.* reference. Since all of the limitations of the invention are not taught by the combination of Li *et al.* and Lemieux, this combination of references does not and cannot render the subject matter of

claims 11-14 and 25 obvious. Applicants request that the rejection of these claims under §103(a) be withdrawn.

Claims 11-14 and 26

Claims 11-14, and 26 stand rejected as allegedly rendered obvious by Li *et al.* in light of Ellis (USPN 5,681,730). Applicants traverse this rejection.

As described in the above section, Li *et al.* does not teach the suppression of *iaaM* in order to prevent a disease caused by *Agrobacterium*. Ellis teaches a method of gymnosperm transformation but does not provide explicit or implicit teachings that overcome the shortcomings of the Li *et al.* reference. Since all of the limitations of the invention are not taught by the combination of Li *et al.* and Ellis, this combination of references does not and cannot render the subject matter of claims 11-14 and 26 obvious. Applicants request that the rejection of these claims under §103(a) be withdrawn.

Claims 11-14 and 28

Claims 11-14 and 28 stand rejected as allegedly rendered obvious by Li *et al.* in light of James *et al.* (1989, Plant Cell Reports 7:658-661) and Lemieux (USPN 5,567,599). Applicants traverse this rejection.

As described in the above section, neither Li *et al.* nor Lemieux teach the suppression of *iaaM* in order to prevent a disease caused by *Agrobacterium*. James *et al.* teaches a method of apple transformation but does not provide explicit or implicit teachings that overcome the shortcomings of the Li *et al.* and the Lemieux references. Since all of the limitations of Applicants' invention are not taught by the combination of Li *et al.*, James *et al.*, and/or Lemieux, this combination of references does not and cannot render the subject matter of claims 11-14 and 28 obvious. Applicants request that the rejection of these claims under §103(a) be withdrawn.

Claim Rejections under 35 U.S.C. §101

Claim 10 stands rejected as allegedly being directed to non-statutory subject matter. As the Examiner suggested, claim 10 has been amended to recite that the seed comprises the nucleic acid molecule used to transform the parent plant cell, therefore Applicants respectfully request that the rejection of this claim be withdrawn.

Claim Rejections under 35 U.S.C. §112, Second Paragraph

Claims 2, 6-7, and 11, and all subsequent dependent claims, stand rejected under 35 U.S.C. §112, second paragraph as allegedly being indefinite for failing to particularly point out and distinctly claim the subject matter which Applicants regard as the invention. Applicants traverse this rejection.

"and fragments thereof"

Claims 2, 6, and 11 are rejected as allegedly being indefinite for not clearly defining "and fragments thereof." Applicants have amended claims 2, 6, and 11 in order to remove this phrase, thereby rendering this rejection moot. Applicants respectfully request that the rejection of these claims be withdrawn.

"reduced" and "reduces"

Claims 6 and 7 are rejected as allegedly being indefinite for not clearly defining "reduced." Claim 11 is rejected as allegedly being indefinite for not clearly defining "reduces." Applicants traverse the rejection. However, in the interest of advancing prosecution, Applicants have amended claims 6, and 7 to recite *a plant resistant to gall disease*. Claim 11 has been amended to recite that the introduction of the recombinant nucleic acid molecule into the plant *makes the plant resistant to gall disease*. The term "resistant" has already been considered by the Examiner in original claim 1 and because it was not objected to, its entry in claims 6, 7, and 11 is appropriate. Applicants respectfully request that the rejection of these claims be withdrawn.

CONCLUSIONS

Based on the foregoing amendments and arguments, the claims are in condition for allowance and notification to this effect is requested. If for any reason the Examiner believes that a telephone conference would expedite allowance of the claims, please telephone the undersigned at (503) 226-7391.

Respectfully submitted,

KLARQUIST SPARKMAN, LLP

By _____
Tanya M. Harding, Ph.D.
Registration No. 42,630

One World Trade Center, Suite 1600
121 S.W. Salmon Street
Portland, Oregon 97204
Telephone: (503) 226-7391
Facsimile: (503) 228-9446

Marked-up Version of Amended Specification and Claims
Pursuant to 37 C.F.R. §§ 1.121(b)-(c)

In the Specification:

On page 1, following the header "GOVERNMENTAL SUPPORT"

--This invention was made with government support under grant numbers 96-34354-3072 and 2002-35319-11555, awarded by the United States Department of Agriculture. The federal government has certain rights in the invention.—

At page 12, first full paragraph

--The present method provides new and effective methods for suppressing the expression of *Agrobacterium* oncogenes. In particular, this invention is directed at, *inter alia*, producing plants that are capable of substantially inhibiting the formation of bacterially induced galls. These plants are produced by selecting a target gene of *Agrobacterium* origin, designing a ~~nucelic~~ nucleic acid (~~typeially~~ typically DNA) BR construct encoding untranslatable single-stranded RNA, double-stranded RNA, and/or untranslatable double-stranded RNA molecules having a high sequence identity to the target gene, and introducing at least one of these BR constructs into a host cell.--

In the Claims:

1. (Once amended) A method of producing a plant cell that is resistant to gall disease, the method comprising transforming a plant cell with ~~at least one~~a nucleic acid molecule that is at least 90% homologous to ~~at least one~~a gene responsible for causing gall disease, wherein the nucleic acid molecule encodes~~encoding an RNA molecule selected from the group consisting of~~ an untranslatable plus-sense RNA molecules, a double-stranded RNA molecules, ~~and~~ or an untranslatable double-stranded RNA molecules, wherein the RNA molecules is at least 700 base pairs in length and comprises at least one stop sequence, and wherein the gene comprises a nucleic acid sequence as set forth as SEQ ID NO: 10, thereby producing a plant cell that is resistant to gall disease.

3. (Once amended) A plant-transformation vector, comprising the nucleic acid molecule of claim ~~2~~1.

6. (Once amended) A method of producing a plant ~~exhibiting a reduced susceptibility~~resistant to gall disease caused by *Agrobacterium*, comprising:

transforming at least one plant cell with at least one nucleic acid molecule that is at least 90% homologous to ~~at least one~~a gene responsible for causing gall disease, ~~or fragment thereof,~~wherein the nucleic acid molecule encodes ~~encoding an RNA molecule selected from the group consisting of~~an untranslatable plus-sense RNA molecules~~,~~ a double-stranded RNA molecules~~, and~~ or an untranslatable double-stranded RNA molecules~~,~~ wherein the RNA molecule is at least 700 base pairs in length and comprises at least one stop sequence, and wherein the gene comprises a nucleic acid sequence as set forth as SEQ ID NO: 10;

growing ~~plants~~ at least one plant from ~~the~~ at least one transformed plant cells~~;~~ and

selecting a plant that shows a reduced susceptibility to gall disease caused by *Agrobacterium*, thereby producing a plant resistant to gall disease caused by *Agrobacterium*.

7. (Once amended) A plant ~~exhibiting a reduced susceptibility~~resistant to gall disease caused by *Agrobacterium*, produced by the method of claim 6.

9. (Once amended) A plant resistant to gall disease produced by sexual or asexual reproduction of the plant of claim 7.

10. (Once amended) A seed produced by selfing or outcrossing the plant of claim 7, wherein the seed comprises the nucleic acid molecule used to transform the plant cell.

11. (Once amended) A recombinant nucleic acid molecule comprising a nucleic acid sequence having at least ~~60~~90% sequence identity with a ~~nucleic acid sequence~~ gene responsible for causing gall disease, wherein the gene comprises a nucleic acid sequence ~~selected from the group consisting of~~as set forth as SEQ ID NO: 10, wherein the nucleic acid sequence encodes an untranslatable plus-sense RNA molecule, a double-stranded RNA molecule, or an untranslatable

double-stranded RNA molecule, wherein the RNA molecules is at least 700 base pairs in length and comprises at least one stop sequence, ~~SEQ ID NO: 11, SEQ ID NO: 12, and fragments thereof,~~ and wherein the recombinant nucleic acid molecule, when introduced into and ~~expressed~~ transcribed in a plant, ~~reduces susceptibility of~~makes the plant resistant to gall disease ~~caused by *Agrobacterium*~~.

41. (New) The method of claim 1, wherein the at least one stop sequence is located at a third codon in the nucleic acid sequence as set forth as SEQ ID NO: 10.

42. (New) The method of claim 41, further comprising a deletion of two nucleotides following the third codon in the nucleic acid sequence as set forth as SEQ ID NO: 10.

43. (New) The method of claim 1, wherein the untranslatable plus-sense RNA molecule, double-stranded RNA molecule, or untranslatable double-stranded RNA molecule is at least 700 base pairs in length and comprises nucleotide residues between positions 1 through 1802 of the nucleic acid sequence as set forth as SEQ ID NO: 10.

44. (New) The method of claim 1, wherein the untranslatable plus-sense RNA molecule, double-stranded RNA molecule, or untranslatable double-stranded RNA molecule is at least 700 base pairs in length and comprises a nucleic acid sequence as set forth as SEQ ID NO: 7.

45. (New) The method of claim 6, wherein the at least one stop sequence is located at a third codon in the nucleic acid sequence as set forth as SEQ ID NO: 10.

46. (New) The method of claim 45, further comprising a deletion of two nucleotides following the third codon in the nucleic acid sequence as set forth as SEQ ID NO: 10.

47. (New) The method of claim 6, wherein the untranslatable plus-sense RNA molecule, double-stranded RNA molecule, or untranslatable double-stranded RNA molecule is at least 700 base pairs in length and comprises nucleotide residues between positions 1 through 1802 of the nucleic acid sequence as set forth as SEQ ID NO: 10.

48. (New) The method of claim 6, wherein the untranslatable plus-sense RNA molecule, double-stranded RNA molecule, or untranslatable double-stranded RNA molecule is at least 700 base pairs in length and comprises a nucleic acid sequence as set forth as SEQ ID NO: 7.

Blast 2 Sequences r sults

PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.4 [Aug-26-2002]

Match: 1 Mismatch: -2 gap open: 5 gap extension: 2

x_dropoff: 50 expect: 10.000 wordsize: 11 Filter ☑ Align

Sequence 1 lcl|seq_1 **Length** 2268 (1 .. 2268)

Sequence 2 lcl|seq_2 **Length** 2268 (1 .. 2268)

NOTE:The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence

```
Score = 3603 bits (1874), Expect = 0.0
Identities = 2140/2268 (94%), Gaps = 2/2268 (0%)
 Strand = Plus / Plus
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```
Query: 1    atgtcagcttcacctctccttgataaccagtgcgatcatctcccaaccaaaatggtggat 60
             ||||||||||| ||||||||||||||||||||||||||| || | ||||||||||||||| 
Sbjct: 1    atgtcagcttcagctctccttgataaccagtgcgatcatttctctaccaaaatggtggat 60

Query: 61   ctgacaatggtcgataaggcggatgaattggaccgcagggtttccgatgccttcttagaa 120
             |||| |||||||||||||| |||||||||||||||||||||||||||||||||| |||| 
Sbjct: 61   ctgataatggtcgataaggctgatgaattggaccgcagggtttccgatgccttctcagaa 120

Query: 121  cgagaagcttctaggggaaggaggattactcaaagctccaccgagtgcagcgctgggtta 180
             || |||||||||||||||||| |||||||||| ||||  |||||||||||||||||||| 
Sbjct: 121  cgtgaagcttctaggggaaggatgattactcaaatctccggcgagtgcagcgctgggtta 180

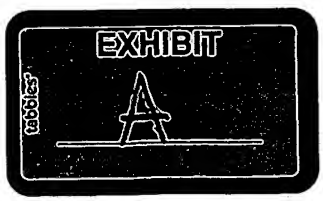
Query: 181  gcttgcaaaaggctggccgatggtcgcttccccgagatctcagctggtggaaaggtagca 240
             |||||||||||||||||||| |||||||| |||||||||||||||||||  ||||||||| 
Sbjct: 181  gcttgcaaaaggctggccgacggtcgctttcccgagatctcagctggtgagaaggtagca 240

Query: 241  gttctctccgcttatatctatattggcaaagaaattctggggcggatacttgaatcgaaa 300
             |  |||||||||| |||||| ||||||| |||||||||||||||||||||||||||| || 
Sbjct: 241  gccctctccgcttacatctatgttggcaaggaaattctggggcggatacttgaatcggaa 300

Query: 301  ccttgggcgcgggcaacagtgagtggtctcgttgccatcgacttggacaccatttgcatg 360
             |||||||||| |||| |||||||||||||||||||||| | |   |  |||| ||| 
Sbjct: 301  ccttgggcgcgagcaagagtgagtggtctcgttgccatcgaccttgcaccattttgtatg 360
```

SEQ ID NO:10 (octopine-type Ti)

nopaline-type Ti



```
Query: 361  gatttctccgaagcacaactaatccaagccctgtttttgctgagcggtaaaagatgtgca 420
            ||||||||||||||||||||  ||||| ||||||||||||||||||||||||||||||||
Sbjct: 361  gatttctccgaagcacaacttctccaaaccctgtttttgctgagcggtaaaagatgtgca 420

Query: 421  ccgattgatcttagtcatttcgtggccatttcaatctctaagactgccggctttcgaacc 480
             | |  ||||||||||||||||||||||||||||||||||||||||||||| |||  ||||||
Sbjct: 421  tccagcgatcttagtcatttcgtggccatttcaatctctaagactgcccgctcccgaacc 480

Query: 481  ctgccaatgccgctgtacgagaatggcacgatgaaatgcgttaccgggtttaccataacc 540
            |||| ||||||||  ||||||||  |||||||  |||| ||||||||||||||||| | |||
Sbjct: 481  ctgcaaatgccgccttacgagaaaggcacgacgaaacgcgttaccgggtttaccctgacc 540

Query: 541  cttgaaggggccgtgccatttgacatggtagcttatggtcgaaacctgatgctgaagggt 600
            ||||||| ||||||  ||||||||||||||||||||||||||||||||||||||||||| |
Sbjct: 541  cttgaagaggccgtaccatttgacatggtagcttatggtcgaaacctgatgctgaaggct 600

Query: 601  tcggcaggttcctttccaacaatcgacttgctctacgactgcagaccgttttttgaccaa 660
            |||||||||||||||||||||  |||||||||||  ||||  ||||  ||||||||||||||
Sbjct: 601  tcggcaggttcctttccaacaattgacttgctctatgactacagatcgttttttgaccaa 660

Query: 661  tgttccgatagtggacggatcggcttctttccggaggatgttcctaagccgaaagtggcg 720
            |||||||||||||||||||||||||||||||||  ||||||||||||||  |||||||||
Sbjct: 661  tgttccgatagtggacggatcggcttctttccggaagatgttcctaagccaaaagtggcg 720

Query: 721  gtcattggcgctggcatttccggactcgtggtggcaaacgaactgcttcatgctggggta 780
             ||||||||||||||||||||||||||||||||||  ||||||||||||||||||  |||
Sbjct: 721  atcattggcgctggcatttccggactcgtggtggcaagcgaactgcttcatgctggtgta 780

Query: 781  gacgatgttacaatatatgaagcaagtgatcgtgttggaggcaagctttggtcacatgct 840
            ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
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Query: 841  ttcagggacgctcctagtgtcgtggccgaaatgggggcgatgcgatttcctcctgctgca 900
            ||||  |||||||||  ||  ||  ||||||||||||||||||||||||||||||||||||
Sbjct: 841  ttcaaggacgctcccagcgtggtggccgaaatgggggcgatgcgatttcctcctgctgca 900

Query: 901  ttctgcttgtttttcttcctcgagcgttacggcctgtcttcgatgaggccgttcccaaat 960
            |  ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||
Sbjct: 901  tcgtgcttgtttttcttcctcgagcggtacggcctgtcttcgatgaggccgttcccaaat 960

Query: 961  cccggcacagtcgacacttacttggtctaccaaggcgtccaatacatgtggaaagccggg 1020
            ||||||||||||||||||  ||||||||||||||||  |||  ||||||||||||||||||
Sbjct: 961  cccggcacagtcgacactaacttggtctaccaaggcctccgatacatgtggaaagccggg 1020

Query: 1021 cagctgccaccgaagctgttccatcgcgtttacaacggttggcgtgcgttcttgaaggac 1080
            ||||  ||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Sbjct: 1021 cagcagccaccgaagctgttccatcgcgtttacagcggttggcgtgcgttcttgaaggac 1080

Query: 1081 ggttttcatgagcgagatattgtgttggcttcgcctgtcgctattactcaggccttgaaa 1140
            |||||  ||||||  ||||||||||||||||||||||||  ||||||||||  |||||||||
Sbjct: 1081 ggtttccatgagggagatattgtgttggcttcgcctgttgctattactcaagccttgaaa 1140

Query: 1141 tcaggacacattaggtgggctcatgactcctggcaaatttggctgaaccgtttcgggagg 1200
            ||||||  ||||||||  ||||||||||||||||||||  ||||||||||||||||||||||
Sbjct: 1141 tcaggagacattaggcgggctcatgactcctggcaaacttggctgaaccgtttcgggagg 1200

Query: 1201 gagtccttctcttcagggatagagaggatctttctgggcacacatcctcctggtggt-aa 1259
            ||||||||||||||  ||||||||||||||||||||||||  ||||||||||||||  ||
Sbjct: 1201 gagtccttctcttcagcgatagagaggatctttctgggcacgcatcctcctggtggtgaa 1260
```

```
Query: 1260 acatggagttttcctcatgattgggacctattcaagctaatgggaataggatctggcggg 1319
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||| ||
Sbjct: 1261 acatggagtttccctcatgattgggacctattcaagctaatgggaataggatctggc-gg 1319

Query: 1320 gtttggtccagtttttgaaagcgggtttattgagatcctccgcttggtcatcaacggata 1379
           |||||||||||||||||||||||||||||||||||||||||| |||||||||| ||||||||
Sbjct: 1320 gtttggtccagtttttgaaagcgggtttattgagatccttcgcttggtcataaacggata 1379

Query: 1380 tgaagaaaatcagcggatgtgccctgaaggaatctcagaacttccacgtcggatcgcatc 1439
           |||||||||||||||||||||| |||||||||||||||||||||||| || ||  |
Sbjct: 1380 tgaagaaaatcagcggatgtgctctgaaggaatctcagaacttccacgtcgaatagccac 1439

Query: 1440 tgaagtggttaacggtgtgtctgtgagccagcgcatatgccatgttcaagtcagggcgat 1499
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Query: 1500 tcagaaggaaaagacaaaaataaagataaggcttaagagcgggatatctgaactttatga 1559
           | |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 1500 tgagaaagaaaagacaaaaataaagataaggcttaagagcgggatatctgaactttatga 1559

Query: 1560 taaggtggtggtcacatctggactcgcaaatatccaactcaggcattgcctgacatgcga 1619
           |||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Sbjct: 1560 taaggtggtggttacatctggactcgcaaatatccaactcaggcattgtctgacatgcga 1619

Query: 1620 taccaatatttttcaggcaccagtgaaccaagcggttgataacagccatatgacaggatc 1679
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           |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Sbjct: 1740 tgtcctcatggacgggatcgcaaaagcagtgtactgcctggactatgagccgcaggatcc 1799

Query: 1800 gaatggtaaaggtctagtgctcatcagttatacatgggaggacgactcccacaagctgtt 1859
           |||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
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Query: 1860 ggcggtccccgacaaaaaagagcgattatgtctgctgcgggacgcaatttcgagatcttt 1919
           |||||| |||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct: 1860 ggcggttcccgacaaaaaagagcgattctgtctgctgcgggacgcaatttcgagatcttt 1919

Query: 1920 cccggcgtttgcccagcacctatttcctgcctgcgctgattacgaccaaaatgttattca 1979
           |||||||||||||||||| ||| |||| ||||||||||||||||||||||||| ||||
Sbjct: 1920 cccggcgtttgcccagcatctagttcccgcctgcgctgattacgaccaaaatgttgttca 1979

Query: 1980 acatgattggcttacagacgagaatgccgggggagctttcaaactcaaccggcgtggtga 2039
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Query: 2040 ggatttttattctgaagaacttttctttcaagcactggacacggctaatgataccggagt 2099
           |||||||||||||||||||||||||||||||| ||||||| | ||||||||||||||||
Sbjct: 2040 ggatttttattctgaagaacttttctttcaagcgctggacatgactaatgataccggagt 2099

Query: 2100 ttacttggcgggttgcagttgttccttcacaggtggatgggtggagggtgctattcagac 2159
           |||||||||||||||||||||||||||||| |||||||||||||||| ||||||||||
Sbjct: 2100 ttacttggcgggttgcagttgttccttcaccggtggatgggtggagggcgctattcagac 2159
```

```
Query: 2160 cgcgtgtaacgccgtctgtgcaattatccacaattgtggaggcattttggcaaagggcaa 2219
           ||||||||||||||||||||||||||||||||||||||||| |||||||||||| |||
Sbjct: 2160 cgcgtgtaacgccgtctgtgcaattatccacaattgtggaggtattttggcaaaggacaa 2219


Query: 2220 tcctctcgaacactcttggaagagatataactaccgcagtagaaatta 2267
           |||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 2220 tcctctcgaacactcttggaagagatataactaccgcaatagaaatta 2267

CPU time:     0.09 user secs.     0.05 sys. secs     0.14 total secs.

Lambda     K      H
    1.33    0.621     1.12

Gapped
Lambda     K      H
    1.33    0.621     1.12


Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Hits to DB: 5
Number of Sequences: 0
Number of extensions: 5
Number of successful extensions: 4
Number of sequences better than 10.0: 1
length of query: 2268
length of database: 7,234,536,489
effective HSP length: 25
effective length of query: 2243
effective length of database: 7,234,536,464
effective search space: 16227065288752
effective search space used: 16227065288752
T: 0
A: 0
X1: 6 (11.5 bits)
X2: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)
```